



IFWO

RAW SEQUENCE LISTING

DATE: 09/10/2004

PATENT APPLICATION: US/10/059,506

TIME: 14:32:33

Input Set : N:\CrF3\RULE60\10059506.raw.txt

Output Set: N:\CRF4\09102004\J059506.raw

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1 <110> APPLICANT: Kelly, Kathleen
2   The Government of the United States of America
3   as represented by The Secretary of the
4   Department of Health and Human Services
5 <120> TITLE OF INVENTION: Methods and Compositions for Inhibiting Inflammation
6   and Angiogenesis Comprising a Mammalian CD97 Alpha
7   Subunit
8 <130> FILE REFERENCE: 015280-263100US
9 <140> CURRENT APPLICATION NUMBER: 10/059,506
10 <141> CURRENT FILING DATE: 2002-01-29
11 <150> PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/09/284,819
W--> 12 <151> PRIOR FILING DATE: FILING DATE: 1999-08-20
13 <150> PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 60/027,871
W--> 14 <151> PRIOR FILING DATE: FILING DATE: 1996-10-25
15 <150> PRIOR APPLICATION NUMBER: APPLICATION NUMBER: WO PCT/US97/19772
W--> 16 <151> PRIOR FILING DATE: FILING DATE: 1997-10-24
17 <160> NUMBER OF SEQ ID NOS: 21
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 42
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Description of Artificial Sequence:EGF-1 EGF-like
26   repeat conserved motif
27 <400> SEQUENCE: 1
28   Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln Asn Ser Ser Cys Val
29       1           5           10           15
30   Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe Ser Ser Phe Ser Glu
31           20           25           30
32   Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp
33       35           40
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 52
37 <212> TYPE: PRT
38 <213> ORGANISM: Artificial Sequence
39 <220> FEATURE:
40 <223> OTHER INFORMATION: Description of Artificial Sequence:EGF-2 EGF-like
41   repeat conserved motif
42 <400> SEQUENCE: 2
43   Asp Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe
44       1           5           10           15
45   Ser Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro

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46          20          25          30
47  Gly Tyr Glu Pro Val Ser Gly Thr Lys Thr Phe Lys Asn Glu Ser Glu
48          35          40          45
49  Asn Thr Cys Gln
50          50
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 44
54 <212> TYPE: PRT
55 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: Description of Artificial Sequence:EGF-3 EGF-like
58  repeat conserved motif
59 <400> SEQUENCE: 3
60  Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys Ser Tyr Gly
61      1          5          10          15
62  Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys Leu Pro Gly
63      20          25          30
64  Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr
65      35          40
67 <210> SEQ ID NO: 4
68 <211> LENGTH: 49
69 <212> TYPE: PRT
70 <213> ORGANISM: Artificial Sequence
71 <220> FEATURE:
72 <223> OTHER INFORMATION: Description of Artificial Sequence:EGF-4 EGF-like
73  repeat conserved motif
74 <400> SEQUENCE: 4
75  Asp Val Asn Glu Cys Thr Ser Gly Gln Asn Pro Cys His Ser Ser Thr
76      1          5          10          15
77  His Cys Leu Asn Asn Val Gly Ser Tyr Gln Cys Arg Cys Arg Pro Gly
78      20          25          30
79  Trp Gln Pro Ile Pro Gly Ser Pro Asn Gly Pro Asn Asn Thr Val Cys
80      35          40          45
81  Glu
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 49
85 <212> TYPE: PRT
86 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
88 <223> OTHER INFORMATION: Description of Artificial Sequence:EGF-5 EGF-like
89  repeat conserved motif
90 <400> SEQUENCE: 5
91  Asp Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr
92      1          5          10          15
93  Val Cys Phe Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys Arg Pro Gly
94      20          25          30
95  Trp Lys Pro Arg His Gly Ile Pro Asn Asn Gln Lys Asp Thr Val Cys
96      35          40          45
97  Glu

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99 <210> SEQ ID NO: 6
100 <211> LENGTH: 835
101 <212> TYPE: PRT
102 <213> ORGANISM: Homo sapiens
103 <220> FEATURE:
104 <223> OTHER INFORMATION: CD97amino acid sequence encoded by full-length
105 clone pAT276
106 <400> SEQUENCE: 6
107 Met Gly Gly Arg Val Phe Leu Ala Phe Cys Val Trp Leu Thr Leu Pro
108      1          5          10          15
109 Gly Ala Glu Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln
110      20          25          30
111 Asn Ser Ser Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe
112      35          40          45
113 Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp
114      50          55          60
115 Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser
116      65          70          75          80
117 Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly
118      85          90          95
119 Tyr Glu Pro Val Ser Gly Thr Lys Thr Phe Lys Asn Glu Ser Glu Asn
120      100         105         110
121 Thr Cys Gln Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys
122      115         120         125
123 Ser Tyr Gly Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys
124      130         135         140
125 Leu Pro Gly Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp
126      145         150         155         160
127 Val Asn Glu Cys Thr Ser Gly Gln Asn Pro Cys His Ser Ser Thr His
128      165         170         175
129 Cys Leu Asn Asn Val Gly Ser Tyr Gln Cys Arg Cys Arg Pro Gly Trp
130      180         185         190
131 Gln Pro Ile Pro Gly Ser Pro Asn Gly Pro Asn Asn Thr Val Cys Glu
132      195         200         205
133 Asp Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr
134      210         215         220
135 Val Cys Phe Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys Arg Pro Gly
136      225         230         235         240
137 Trp Lys Pro Arg His Gly Ile Pro Asn Asn Gln Lys Asp Thr Val Cys
138      245         250         255
139 Glu Asp Met Thr Phe Ser Thr Trp Thr Pro Pro Pro Gly Val His Ser
140      260         265         270
141 Gln Thr Leu Ser Arg Phe Phe Asp Lys Val Gln Asp Leu Gly Arg Asp
142      275         280         285
143 Ser Lys Thr Ser Ser Ala Glu Val Thr Ile Gln Asn Val Ile Lys Leu
144      290         295         300
145 Val Asp Glu Leu Met Glu Ala Pro Gly Asp Val Glu Ala Leu Ala Pro
146      305         310         315         320
147 Pro Val Arg His Leu Ile Ala Thr Gln Leu Leu Ser Asn Leu Glu Asp

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148				325				330				335				
149	Ile	Met	Arg	Ile	Leu	Ala	Lys	Ser	Leu	Pro	Lys	Gly	Pro	Phe	Thr	Tyr
150				340				345				350				
151	Ile	Ser	Pro	Ser	Asn	Thr	Glu	Leu	Thr	Leu	Met	Ile	Gln	Glu	Arg	Gly
152			355				360				365					
153	Asp	Lys	Asn	Val	Thr	Met	Gly	Gln	Ser	Ser	Ala	Arg	Met	Lys	Leu	Asn
154		370				375				380						
155	Trp	Ala	Val	Ala	Ala	Gly	Ala	Glu	Asp	Pro	Gly	Pro	Ala	Val	Ala	Gly
156	385				390				395			400				
157	Ile	Leu	Ser	Ile	Gln	Asn	Met	Thr	Thr	Leu	Leu	Ala	Asn	Ala	Ser	Leu
158				405				410				415				
159	Asn	Leu	His	Ser	Lys	Lys	Gln	Ala	Glu	Leu	Glu	Glu	Ile	Tyr	Glu	Ser
160			420				425				430					
161	Ser	Ile	Arg	Gly	Val	Gln	Leu	Arg	Arg	Leu	Ser	Ala	Val	Asn	Ser	Ile
162		435				440				445						
163	Phe	Leu	Ser	His	Asn	Asn	Thr	Lys	Glu	Leu	Asn	Ser	Pro	Ile	Leu	Phe
164	450				455			460								
165	Ala	Phe	Ser	His	Leu	Glu	Ser	Ser	Asp	Gly	Glu	Ala	Gly	Arg	Asp	Pro
166	465			470				475				480				
167	Pro	Ala	Lys	Asp	Val	Met	Pro	Gly	Pro	Arg	Gln	Glu	Leu	Leu	Cys	Ala
168			485				490				495					
169	Phe	Trp	Lys	Ser	Asp	Ser	Asp	Arg	Gly	Gly	His	Trp	Ala	Thr	Glu	Gly
170			500				505				510					
171	Cys	Gln	Val	Leu	Gly	Ser	Lys	Asn	Gly	Ser	Thr	Thr	Cys	Gln	Cys	Ser
172		515				520					525					
173	His	Leu	Ser	Ser	Phe	Ala	Ile	Leu	Met	Ala	His	Tyr	Asp	Val	Glu	Asp
174	530				535			540								
175	Trp	Lys	Leu	Thr	Leu	Ile	Thr	Arg	Val	Gly	Leu	Ala	Leu	Ser	Leu	Phe
176	545			550				555				560				
177	Cys	Leu	Leu	Leu	Cys	Ile	Leu	Thr	Phe	Leu	Leu	Val	Arg	Pro	Ile	Gln
178			565				570				575					
179	Gly	Ser	Arg	Thr	Thr	Ile	His	Leu	His	Leu	Cys	Ile	Cys	Leu	Phe	Val
180			580			585					590					
181	Gly	Ser	Thr	Ile	Phe	Leu	Ala	Gly	Ile	Glu	Asn	Glu	Gly	Gly	Gln	Val
182		595				600					605					
183	Gly	Leu	Arg	Cys	Arg	Leu	Val	Ala	Gly	Leu	Leu	His	Tyr	Cys	Phe	Leu
184		610				615					620					
185	Ala	Ala	Phe	Cys	Trp	Met	Ser	Leu	Glu	Gly	Leu	Glu	Leu	Tyr	Phe	Leu
186	625				630			635				640				
187	Val	Val	Arg	Val	Phe	Gln	Gly	Gln	Gly	Leu	Ser	Thr	Arg	Trp	Leu	Cys
188			645				650					655				
189	Leu	Ile	Gly	Tyr	Gly	Val	Pro	Leu	Leu	Ile	Val	Gly	Val	Ser	Ala	Ala
190			660				665					670				
191	Ile	Tyr	Ser	Lys	Gly	Tyr	Gly	Arg	Pro	Arg	Tyr	Cys	Trp	Leu	Asp	Phe
192		675				680					685					
193	Glu	Gln	Gly	Phe	Leu	Trp	Ser	Phe	Leu	Gly	Pro	Val	Thr	Phe	Ile	Ile
194		690				695					700					
195	Leu	Cys	Asn	Ala	Val	Ile	Phe	Val	Thr	Thr	Val	Trp	Lys	Leu	Thr	Gln
196	705				710					715						720

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197   Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg
198               725               730               735
199   Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys Thr
200               740               745               750
201   Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu Thr
202               755               760               765
203   Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr Leu
204               770               775               780
205   Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys Trp
206               785               790               795               800
207   Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser Thr
208               805               810               815
209   Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser Glu
210               820               825               830
211   Ser Gly Ile
212               835
214 <210> SEQ ID NO: 7
215 <211> LENGTH: 3
216 <212> TYPE: PRT
217 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Description of Artificial Sequence:RGD motif
220   binding site for several classes of integrins
221 <400> SEQUENCE: 7
222   Arg Gly Asp
223       1
225 <210> SEQ ID NO: 8
226 <211> LENGTH: 3156
227 <212> TYPE: DNA
228 <213> ORGANISM: Homo sapiens
229 <220> FEATURE:
230 <223> OTHER INFORMATION: full length pAT276 encoding CD97
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (49)..(2556)
234 <223> OTHER INFORMATION: CD97
235 <400> SEQUENCE: 8
236   ctgtcccaact cactctttcc cctgccgctc ctgccggcag ctccaaccat gggaggccgc 60
237   gtctttctcg cattctgtgt ctggctgact ctgccgggag ctgaaaccca ggactccagg 120
238   ggctgtgccc ggtggtgccc tcagaactcc tcgtgtgtca atgccaccgc ctgtcgctgc 180
239   aatccagggt tcagctcttt ttctgagatc atcaccaccc cgacggagac ttgtgacgac 240
240   atcaacgagt gtgcaacacc gtcgaaagtg tcatgcgga aattctcgga ctgctggaac 300
241   acagagggga gctacgactg cgtgtgcagc cgggatatg agcctgttc tgggacaaaa 360
242   acattcaaga atgagagcga gaacacctgt caagatgtgg acgaatgtca gcagaaccca 420
243   aggctctgta aaagctacgg cacctgcgtc aacacccttg gcagctatac ctgccagtgc 480
244   ctgcctggct tcaagttcat acctgaggat ccgaaggctt gcacagatgt gaatgaatgc 540
245   acctccggac aaaatccgtg ccacagctcc acccactgcc tcaacaacgt gggcagctat 600
246   cagtgtcgct gccgaccggg ctggcaaccg attccggggt ccccaatgg cccaaacaat 660
247   accgtctgtg aagatgtgga cgagtgcagc tccgggcagc atcagtgtga cagctccacc 720

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/10/2004
 PATENT APPLICATION: US/10/059,506 TIME: 14:32:34

Input Set : N:\Crf3\RULE60\10059506.raw.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; Xaa Pos. 6,7,8,9,10,11,13,14,16,18,21,25,27,29,30,33,34,35,36,37
 Seq#:19; Xaa Pos. 38,39,40
 Seq#:20; Xaa Pos. 6,7,8,9,10,11,13,14,15,16,17,19,21,22,24,26,28,30,31,34
 Seq#:20; Xaa Pos. 35,36,37,38,39,40,41,42,43,44,45,46,47
 Seq#:21; Xaa Pos. 2,3,4,5,6,7,8,9,11

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10059506.raw.txt

Output Set: N:\CRF4\09102004\J059506.raw

L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
 L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
 L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
 L:404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
 M:341 Repeated in SeqNo=19
 L:423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
 M:341 Repeated in SeqNo=20
 L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0